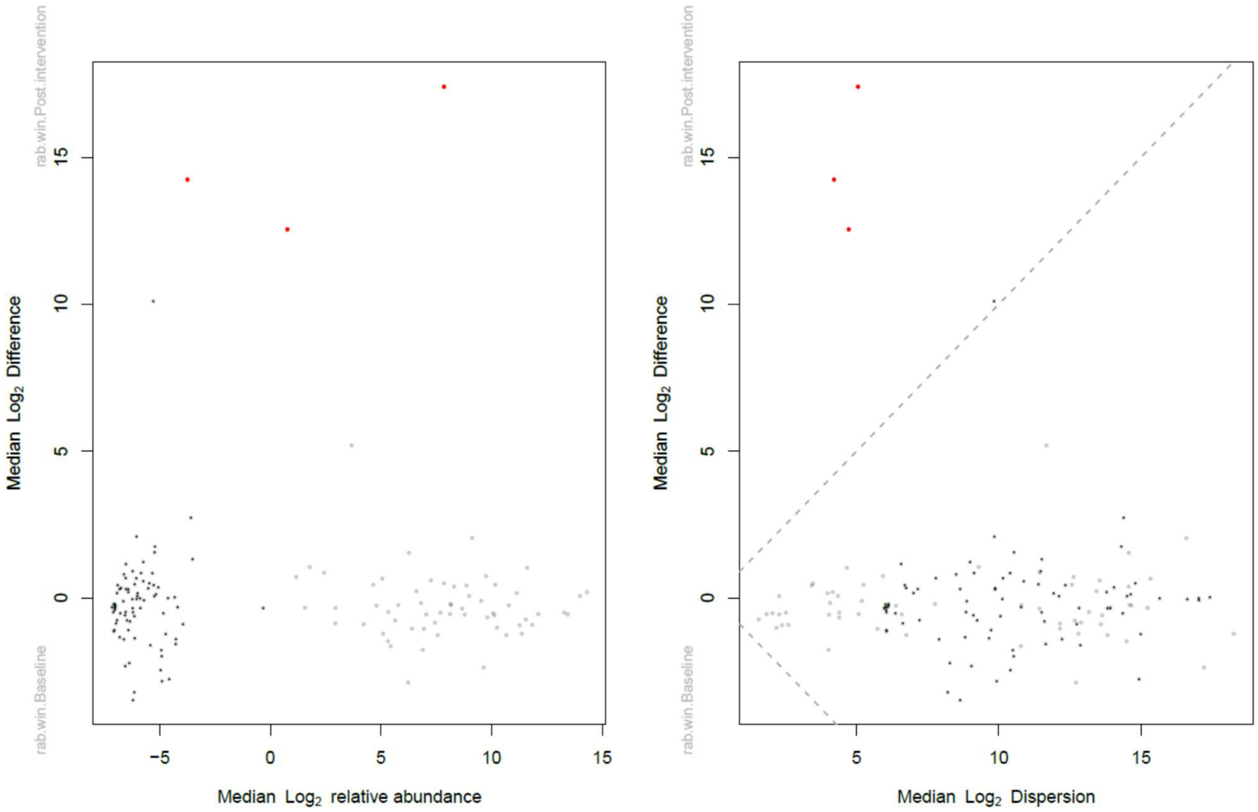
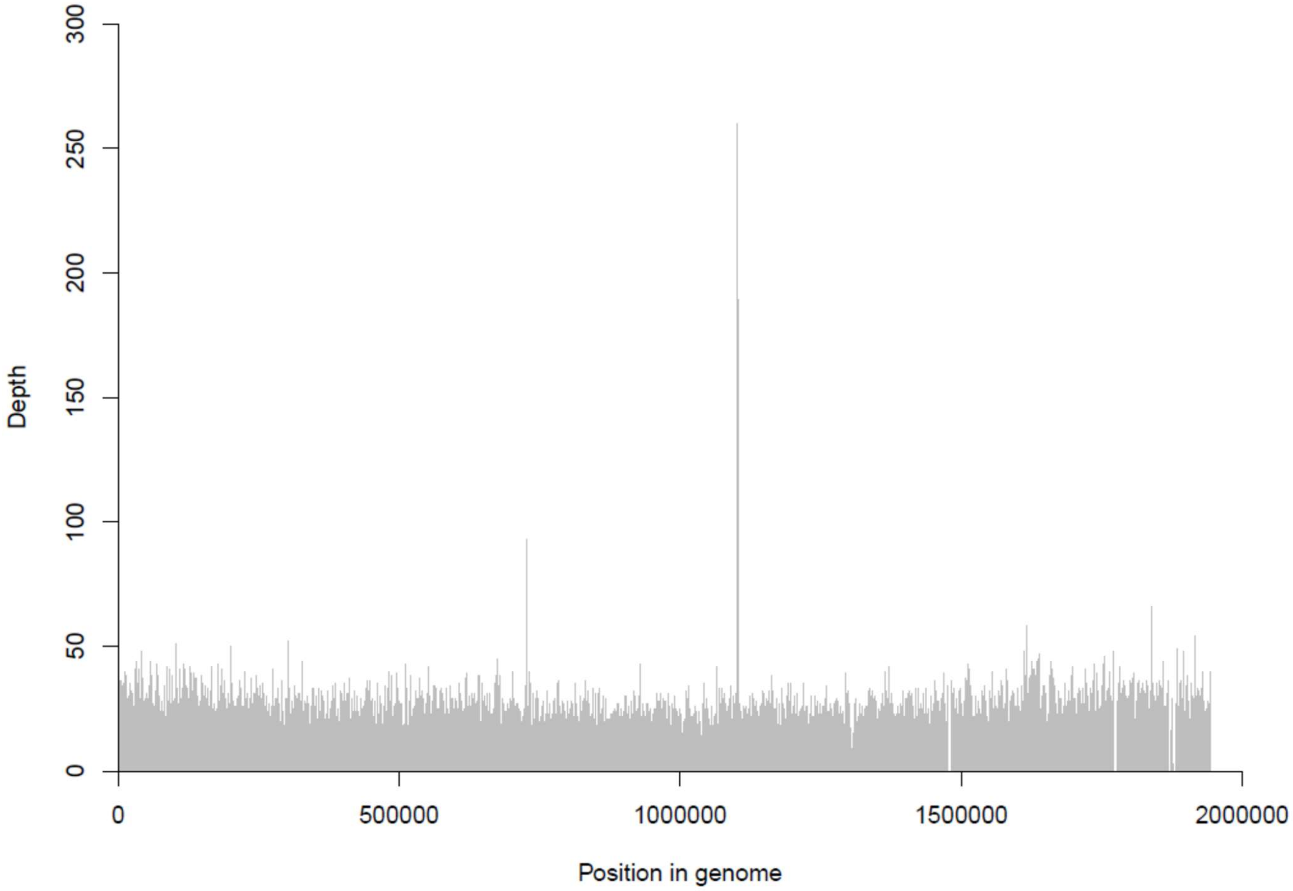
Supplementary material



Supplementary figure 1. ALDex2 differential abundance analysis

Left: MA (Bland-Altman style) plot, right: MW (effect) plot. Red dots represent species called as differentially abundant with $q < 0.1$ (Benjamini-Hochberg corrected P value of Welch's t test), grey dots represent abundant, but not non-differentially abundant species, while black dots represent rare, but not differentially abundant species.



Supplementary figure 2: ***B. animalis*** **subsp.** ***lactis*** **BB-12 coverage plot**

Representative plot showing genome coverage (x-axis) and mapping depth (y-axis) when mapping the sequencing reads of one of the metagenomic samples to *B. animalis* subsp. *lactis* BB-12 (NC_017214).

Supplementary table 2. Genome coverage and depth of the four probiotic organisms.

	Lactobacillus rhamnosus		*Lactobacillus acidophilus*		*L. paracasei* subsp. *paracasei*		*Bifidobacterium animalis* subsp. *lactis*	
Sample	**Coverage**	**Depth**	**Coverage**	**Depth**	**Coverage**	**Depth**	**Coverage**	**Depth**
Subject 1 - B	0.02	1.2			0.03	1.1	0.47	7.2
Subject 2 - B	0.01	1.0			0.06	1.1	0.50	17
Subject 3 - B	0.04	1.2	13.2	1.2	0.17	1.4	0.26	22
Subject 4 - B	0.50	1.7	0.02	1.0	20.8	1.3	0.32	17
Subject 5 - B	0.00	2.0	3.84	1.1			86.9	3.3
Subject 7 - B	0.01	1.2			0.02	1.0	0.37	83
Subject 8 - B	0.03	1.6	0.26	1.3	0.26	2.2	0.16	104
Subject 9 - B					0.11	1.1	0.66	39
Subject 10 - B	0.01	1.8	0.01	1.0	0.39	1.2	0.17	106
Subject 11 - B	0.13	1.1	0.22	1.2	0.05	1.0	17.9	1.5
Subject 12 - B	0.00	2.0			0.17	1.3	0.17	46
Subject 13 - B	0.13	1.2			0.66	1.1	0.40	48
Subject 14 - B	0.06	1.2			0.09	1.1	0.36	40
Subject 15 - B	0.00	2.0			0.00	2.0	1.34	13
Subject 1 - PI	13.4	1.2	40.5	1.4	7.13	1.1	98.5	9.5
Subject 2 - PI	44.0	1.5	42.2	1.5	14.3	1.2	98.6	12
Subject 3 - PI	18.8	1.2	16.7	1.2	0.92	1.1	95.7	4.4
Subject 4 - PI	74.2	2.1	70.3	2.1	15.1	1.3	98.8	28
Subject 5 - PI	61.4	1.8	7.55	1.1	26.3	1.4	97.9	6.4
Subject 7 - PI	31.0	1.3	6.08	1.1	14.4	1.2	87.4	2.9
Subject 8 - PI	20.4	1.2	8.17	1.1	6.24	1.2	88.5	3.0
Subject 9 - PI	58.9	1.7	23.4	1.2	15.2	1.2	98.6	12
Subject 10 - PI	27.6	1.5	58.8	2.0	1.91	1.3	97.4	6.6
Subject 11 - PI	53.3	1.9	79.9	2.9	1.11	1.7	96.3	5.6
Subject 12 - PI	18.1	1.4	30.2	1.5	13.5	1.4	97.5	6.8
Subject 13 - PI	14.6	1.3	10.3	1.3	0.63	1.3	98.5	15
Subject 14 - PI	48.9	1.5	54.9	1.6	22.3	1.2	98.8	27
Subject 15 - PI	0.08	1.1			0.05	1.3	3.56	3.9

A. Genome coverage in percent and the mean read mapping depth from mapping of the metagenomic reads to the four probiotic organisms are shown for the samples from the 14 subjects at first sampling (baseline, B) and the second sampling (post intervention, PI).

	Lactobacillus rhamnosus		***Lactobacillus acidophilus***		***L. paracasei* subsp. *paracasei***		***Bifidobacterium animalis* subsp. *lactis***	
Sample	**Coverage**	**Depth**	**Coverage**	**Depth**	**Coverage**	**Depth**	**Coverage**	**Depth**
Subject 1 - B	0.02	1.2			0.02	1.2	0.35	8.1
Subject 2 - B					0.06	1.1	0.48	14
Subject 3 - B	0.02	1.4	5.92	1.1	0.07	1.2	0.18	16
Subject 4 - B	0.39	1.6	0.02	1.0	15.8	1.2	0.26	14
Subject 5 - B	0.00	2.0	3.59	1.1			85.4	3.1
Subject 7 - B	0.01	1.2			0.02	1.0	0.36	79
Subject 8 - B	0.02	1.1	0.10	1.3	0.13	1.6	0.15	42
Subject 9 - B					0.05	1.0	0.55	28
Subject 10 - B					0.18	1.2	0.15	50
Subject 11 - B	0.07	1.1	0.11	1.1	0.04	1.1	11.2	1.4
Subject 12 - B	0.00	2.0			0.17	1.3	0.17	45
Subject 13 - B	0.06	1.2			0.23	1.1	0.29	27
Subject 14 - B	0.03	1.3			0.07	1.1	0.31	29
Subject 15 - B							0.93	7
Subject 1 - PI	9.07	1.1	29.0	1.3	4.96	1.1	97.7	6.2
Subject 2 - PI	24.0	1.2	23.7	1.3	6.99	1.1	97.2	5
Subject 3 - PI	11.2	1.1	9.71	1.1	0.47	1.1	86.4	2.7
Subject 4 - PI	65.0	1.9	61.7	1.8	12.1	1.3	98.7	22
Subject 5 - PI	53.0	1.6	6.04	1.1	21.9	1.3	96.8	5.1
Subject 7 - PI	26.8	1.3	5.26	1.1	12.5	1.2	83.1	2.6
Subject 8 - PI	18.9	1.2	7.55	1.1	5.77	1.2	86.8	2.8
Subject 9 - PI	48.2	1.5	18.3	1.2	11.6	1.2	98.4	9
Subject 10 - PI	15.1	1.4	37.3	1.6	0.95	1.3	90.6	3.7
Subject 11 - PI	29.6	1.5	53.7	1.9	0.54	1.5	83.3	2.9
Subject 12 - PI	10.6	1.3	18.0	1.4	7.80	1.3	92.0	3.9
Subject 13 - PI	8.48	1.3	6.10	1.2	0.43	1.2	98.2	8
Subject 14 - PI	17.0	1.2	18.8	1.2	6.63	1.1	98.3	7
Subject 15 - PI	0.06	1.1			0.01	1.5	2.37	3.4

B. Genome coverage in percent and the mean read mapping depth when subsampling the human depleted reads to 6 million read pairs, to account for uneven sequencing depth of the samples.

Supplementary table 4. SNP analysis of *B. animalis* subsp. *lactis* strains identified in the subjects

			***B. animalis* subsp. *lactis* BB12 (NC_017214)**					
Sample	**Coverage**	**Depth**	**SNPs**	**Indels**	**SNPs 2x depth**	**Indels 2x depth**	**Depth at SNP positions**	**Variant allele freq.**
Probiotic strain	1921345	82	0	0				
Subject 1 - PI	1915492	10	23	0	2	0	15-16	50-53%
Subject 2 - PI	1917785	12	47	1	5	1	11-22	50-67%
Subject 4 - PI	1919920	28	35	0	15	0	25-56	50-71%
Subject 9 - PI	1916768	12	171	0	60	0	11-23	50-82%
Subject 13 - PI	1915091	15	66	0	15	0	13-27	50-67%
Subject 14 - PI	1921319	27	47	0	2	0	28-35	50-51%

The table shows the genome coverage in bp, mean read mapping depth, number of SNPs and indels for the included samples and the reads from sequencing of probiotic strain when mapping to *Bifidobacterium animalis* subsp. *lactis* BB-12 (NC_017214). The number of SNPs and indels are also shown after removing variants found at >2x mean depth. The variant allele frequency represents the percentage of reads being different from the reference at the SNP positions.